

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973,451

DATE: 12/04/2001

TIME: 20:18:50

Input Set : N:\Crf3\RULE60\09973451.raw

Output Set: N:\CRF3\12042001\I973451.raw

PS

ENTERED

1 <110> APPLICANT: JACOBSON, Myron K.
2 JACOBSON, Elaine L.
3 AM, Jean-Christophe
4 LIN, Winston
5 <120> TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE
6 (PARG) ENZYMES,
7 THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
8 THEREWITH
9 <130> FILE REFERENCE: NIAD 201
10 <140> CURRENT APPLICATION NUMBER: 09/973,451
11 <141> CURRENT FILING DATE: 2001-10-09
12 <150> PRIOR APPLICATION NUMBER: US/09/302,812
13 <151> PRIOR FILING DATE: 1999-04-30
14 <150> PRIOR APPLICATION NUMBER: 60/083,768
15 <151> PRIOR FILING DATE: 1998-05-01
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19 <211> LENGTH: 4070
20 <212> TYPE: DNA
21 <213> ORGANISM: Bos taurus
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35 ttgataagtc accagttgaa aaaggtaac agtatttgaa gcagcatcag actgcggcta 720
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94 <211> LENGTH: 977
95 <212> TYPE: PRT
96 <213> ORGANISM: Bos taurus
97 <220> FEATURE:
98 <400> SEQUENCE: 2

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103     Pro Gly Arg Gln Arg Arg Val Leu Asp Ser Lys Asp Ala Pro Val Gln
104           35          40          45
105     Phe Arg Val Pro Pro Ser Ser Ser Gly Cys Ala Leu Gly Arg Ala Gly
106           50          55          60
107     Gln His Arg Gly Ser Ala Thr Ser Leu Val Phe Lys Gln Lys Thr Ile
108           65          70          75          80
109     Thr Ser Trp Met Asp Thr Lys Gly Ile Lys Thr Val Glu Ser Glu Ser
110           85          90          95
111     Leu His Ser Lys Glu Asn Asn Asn Thr Arg Glu Glu Ser Met Met Ser
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113     Ser Val Gln Lys Asp Asn Phe Tyr Gln His Asn Met Glu Lys Leu Glu
114           115         120         125
115     Asn Val Ser Gln Leu Gly Phe Asp Lys Ser Pro Val Glu Lys Gly Thr
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117     Gln Tyr Leu Lys Gln His Gln Thr Ala Ala Met Cys Lys Trp Gln Asn
118           145         150         155         160
119     Glu Gly Pro His Ser Glu Arg Leu Leu Glu Ser Glu Pro Pro Ala Val
120           165         170         175
121     Thr Leu Val Pro Glu Gln Phe Ser Asn Ala Asn Val Asp Gln Ser Ser
122           180         185         190
123     Pro Lys Asp Asp His Ser Asp Thr Asn Ser Glu Glu Ser Arg Asp Asn
124           195         200         205
125     Gln Gln Phe Leu Thr His Val Lys Leu Ala Asn Ala Lys Gln Thr Met
126           210         215         220
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128           225         230         235         240
129     Ala Cys His Pro Ala Glu Ala Cys Ala Gly Cys Gln Gln Glu Glu Thr
130           245         250         255
131     Asp Val Val Ser Glu Ser Pro Leu Ser Asp Thr Gly Ser Glu Asp Val
132           260         265         270
133     Gly Thr Gly Leu Lys Asn Ala Asn Arg Leu Asn Arg Gln Glu Ser Ser
134           275         280         285
135     Leu Gly Asn Ser Pro Pro Phe Glu Lys Glu Ser Glu Pro Glu Ser Pro
136           290         295         300
137     Met Asp Val Asp Asn Ser Lys Asn Ser Cys Gln Asp Ser Glu Ala Asp
138           305         310         315         320
139     Glu Glu Thr Ser Pro Gly Phe Asp Glu Gln Glu Asp Ser Ser Ser Ala
140           325         330         335
141     Gln Thr Ala Asn Lys Pro Ser Arg Phe Gln Pro Arg Glu Ala Asp Thr
142           340         345         350
143     Glu Leu Arg Lys Arg Ser Ser Ala Lys Gly Gly Glu Ile Arg Leu His
144           355         360         365
145     Phe Gln Phe Glu Gly Gly Glu Ser Arg Ala Gly Met Asn Asp Val Asn
146           370         375         380
147     Ala Lys Arg Pro Gly Ser Thr Ser Ser Leu Asn Val Glu Cys Arg Asn

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148	385	390	395	400
149	Ser Lys Gln His Gly Arg Lys Asp Ser Lys Ile Thr Asp His Phe Met			
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151	Arg Val Pro Lys Ala Glu Asp Lys Arg Lys Glu Gln Cys Glu Met Lys			
152		420	425	430
153	His Gln Arg Thr Glu Arg Lys Ile Pro Lys Tyr Ile Pro Pro His Leu			
154		435	440	445
155	Ser Pro Asp Lys Lys Trp Leu Gly Thr Pro Ile Glu Glu Met Arg Arg			
156		450	455	460
157	Met Pro Arg Cys Gly Ile Arg Leu Pro Pro Leu Arg Pro Ser Ala Asn			
158		465	470	475
159	His Thr Val Thr Ile Arg Val Asp Leu Leu Arg Ile Gly Glu Val Pro			
160		485	490	495
161	Lys Pro Phe Pro Thr His Phe Lys Asp Leu Trp Asp Asn Lys His Val			
162		500	505	510
163	Lys Met Pro Cys Ser Glu Gln Asn Leu Tyr Pro Val Glu Asp Glu Asn			
164		515	520	525
165	Gly Glu Arg Ala Ala Gly Ser Arg Trp Glu Leu Ile Gln Thr Ala Leu			
166		530	535	540
167	Leu Asn Arg Leu Thr Arg Pro Gln Asn Leu Lys Asp Ala Ile Leu Lys			
168		545	550	555
169	Tyr Asn Val Ala Tyr Ser Lys Lys Trp Asp Phe Thr Ala Leu Ile Asp			
170		565	570	575
171	Phe Trp Asp Lys Val Leu Glu Glu Ala Glu Ala Gln His Leu Tyr Gln			
172		580	585	590
173	Ser Ile Leu Pro Asp Met Val Lys Ile Ala Leu Cys Leu Pro Asn Ile			
174		595	600	605
175	Cys Thr Gln Pro Ile Pro Leu Leu Lys Gln Lys Met Asn His Ser Ile			
176		610	615	620
177	Thr Met Ser Gln Glu Gln Ile Ala Ser Leu Leu Ala Asn Ala Phe Phe			
178		625	630	635
179	Cys Thr Phe Pro Arg Arg Asn Ala Lys Met Lys Ser Glu Tyr Ser Ser			
180		645	650	655
181	Tyr Pro Asp Ile Asn Phe Asn Arg Leu Phe Glu Gly Arg Ser Ser Arg			
182		660	665	670
183	Lys Pro Glu Lys Leu Lys Thr Leu Phe Cys Tyr Phe Arg Arg Val Thr			
184		675	680	685
185	Glu Lys Lys Pro Thr Gly Leu Val Thr Phe Thr Arg Gln Ser Leu Glu			
186		690	695	700
187	Asp Phe Pro Glu Trp Glu Arg Cys Glu Lys Leu Leu Thr Arg Leu His			
188		705	710	715
189	Val Thr Tyr Glu Gly Thr Ile Glu Gly Asn Gly Gln Gly Met Leu Gln			
190		725	730	735
191	Val Asp Phe Ala Asn Arg Phe Val Gly Gly Gly Val Thr Ser Ala Gly			
192		740	745	750
193	Leu Val Gln Glu Glu Ile Arg Phe Leu Ile Asn Pro Glu Leu Ile Val			
194		755	760	765
195	Ser Arg Leu Phe Thr Glu Val Leu Asp His Asn Glu Cys Leu Ile Ile			
196		770	775	780

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197 Thr Gly Thr Glu Gln Tyr Ser Glu Tyr Thr Gly Tyr Ala Glu Thr Tyr
198 785 790 795 800
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200 805 810 815
201 Arg Arg Thr Thr Glu Ile Val Ala Ile Asp Ala Leu His Phe Arg Arg
202 820 825 830
203 Tyr Leu Asp Gln Phe Val Pro Glu Lys Ile Arg Arg Glu Leu Asn Lys
204 835 840 845
205 Ala Tyr Cys Gly Phe Leu Arg Pro Gly Val Ser Ser Glu Asn Leu Ser
206 850 855 860
207 Ala Val Ala Thr Gly Asn Trp Gly Cys Gly Ala Phe Gly Gly Asp Ala
208 865 870 875 880
209 Arg Leu Lys Ala Leu Ile Gln Ile Leu Ala Ala Ala Val Ala Glu Arg
210 885 890 895
211 Asp Val Val Tyr Phe Thr Phe Gly Asp Ser Glu Leu Met Arg Asp Ile
212 900 905 910
213 Tyr Ser Met His Thr Phe Leu Thr Glu Arg Lys Leu Thr Val Gly Glu
214 915 920 925
215 Val Tyr Lys Leu Leu Leu Arg Tyr Tyr Asn Glu Glu Cys Arg Asn Cys
216 930 935 940
217 Ser Thr Pro Gly Pro Asp Ile Lys Leu Tyr Pro Phe Ile Tyr His Ala
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233 ttcggacgcc cggagctttc cgagcaggca gaggcgcgtc ctcgaccca aggacgctca 300
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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09973451.raw

Output Set: N:\CRF3\12042001\I973451.raw

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L:946 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
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L:946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:964 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:964 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:964 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:981 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1165 M:256 W: Invalid Numeric Header Field, <220> has non-blank data